

ECCC MAC116

ALLELE 1: 1 GAATTCcGGTTATCTCAGACAAC

ACGATCGCTTAAAGACACGATTAT

ALLELE 2: 1 GAATTCTGGTTATCTCAGACAACCTTGTGTTGGTATTAAGTAAAGCAAGCT

-----MFE-----AAGTCTCTTAA

ALLELE 1: 60 CCAGGCTTGAGAGGCATAGAAATAAATTATTAAlaAaAAAAAACACACAC

AIJ.ELE 2: 60 CCAGGCTTGAGAGGCATAGAAATAATTTTATAAT--AAAAHHAGCCTCTT

EATG MCGA 87

Allele 1: 1 GAATTCATGGTTTCTCTTAT-----GACATTGTTGCCAAGTAATACTAATAATAATCTCAATCT

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Allele 2: 1 GAATTCATGGTTTCTTATCtcttatGACAT

Allele 1: 68 CTGATAACCGTGGTCGTTAA 87

Eccc MATG161

ALLENLE1: 1 TTAAATGAAAAATCGATCAAAATCAAATAATATATAGCTTTTATTAGTAG-9GTTCACCT

CTTCAAGTACT

ALLELE2: 1 TTAAATGAAAATCGATCAAAATCAAATAAATAAGCTTTT

116

ALLELE1: 61 TTTT TTTTATTTGAAAAAATCGACCCCAAGTTGAAACAACATGTTTGAGAAATCTGTTC

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Allele2: 62 TTTT TTTAT TGAAAAAATCGACCCAAAGT TGAACACATG TTAGAAATGTTTC

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AYJFELE1: 117 GCATCCAACGTTTTTCTTGTAACAATCAGCTGTGAGAGGGGAATTC TGT

AIJ.EI.E2: 118 GCATCCAACGTTTTTCTTGTACAATCAGCTGTGAGAGGGGAATTC 162

ECCAMAGC114

ALLELE1: 1 GAATTC CAGC - AGATTGTATCAACAAGTATGTCACATTTCTGTT

TTTCTGAGCATTATTA 59

ALLELE2: 1 GAATCCCAG-CtAGATTGTGTATCAACAATGTAIGTCCACAAATGTCATGCT

-----GGGCGAGCCGACCTGTGCCTTAA 174

ALLELE1: 60 GGGAACGCTATTCTTACTTCTAAATTTTATIGACAATCCAAAGTGTGCTTTT

114

ALLELE2: 60 GGGAAC TGTAT TCTTACT TCTAAAT TTTTAT TIGACA TCCAAAG TGTGCT...

b.
E_{ATG}M_{CGA}87 BAC extension and TaqMan probe and primers

Allele 1:	ttatcatccaaaaattaaaaattgaaaaactttaatacaaaatgcacattttggagccattcatgtc
Allele 2:	ttatcatccaaaaattaaaaattgaaaaactttaatacaaaatgcacattttggagccattcatgtc <i>TMA5-RE</i>
Allele 1:	<u><i>TMA5F</i></u> atctcttggtctgagtccttatcattctgtggattGAATTCAATGGTTCTCTTAT-----GACATTGTT
Allele 2:	atctcttggtctgagtccttatcattctgtggattGAATTCAATGGTTCTCTTATcttatGACATTGTT <i>TMA5-R</i>
Allele 1:	GCCAAGTAATACTACTATATAAAATTCAGATTGGGTTTCTGATAACCGTGGTCGTTAAactatataataacc
Allele 2:	GCCAAGTAATACTACTATATAAAATTCAGATTGGGTTTCTGATAACCGTGGTCGTTAAactatataataacc <u>ATG4BACF</u>

Figure 2

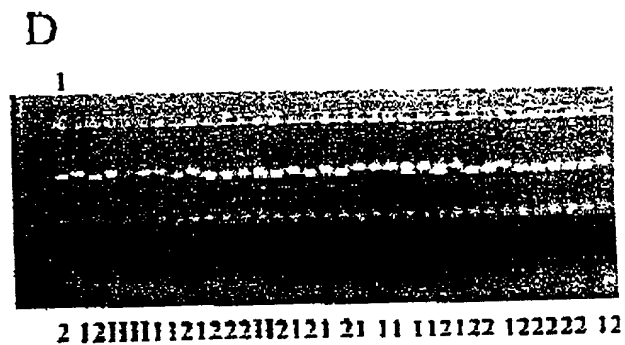
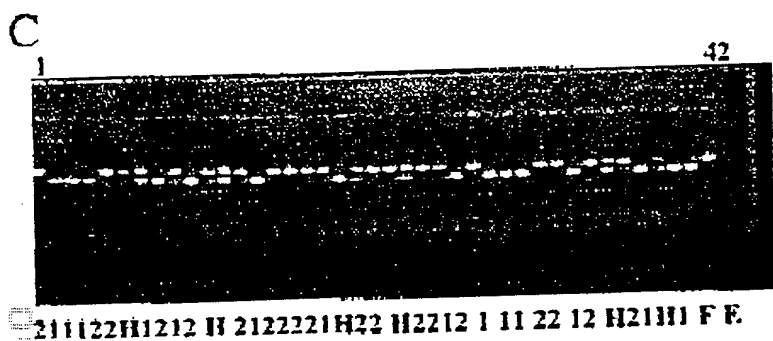
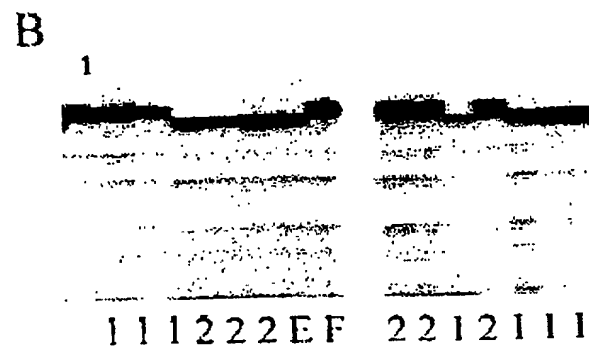
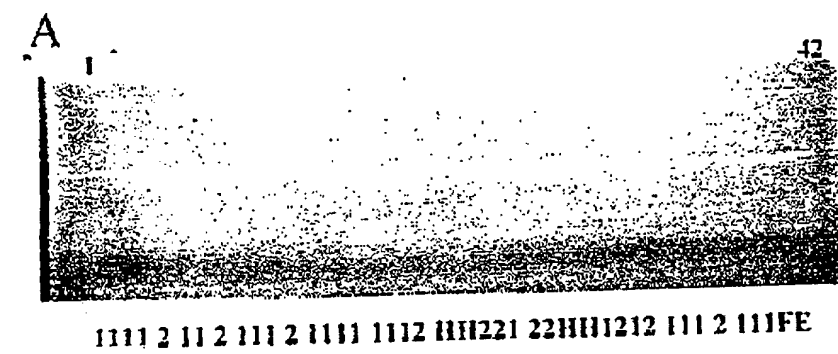


Figure 3

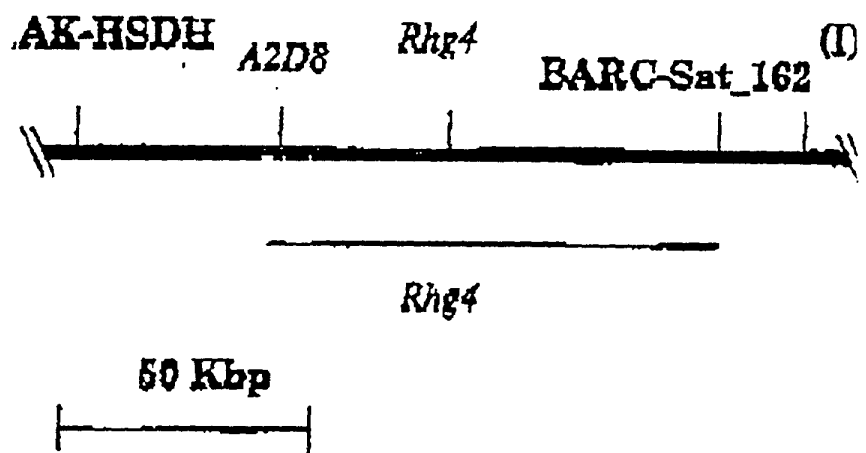
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Figure 4

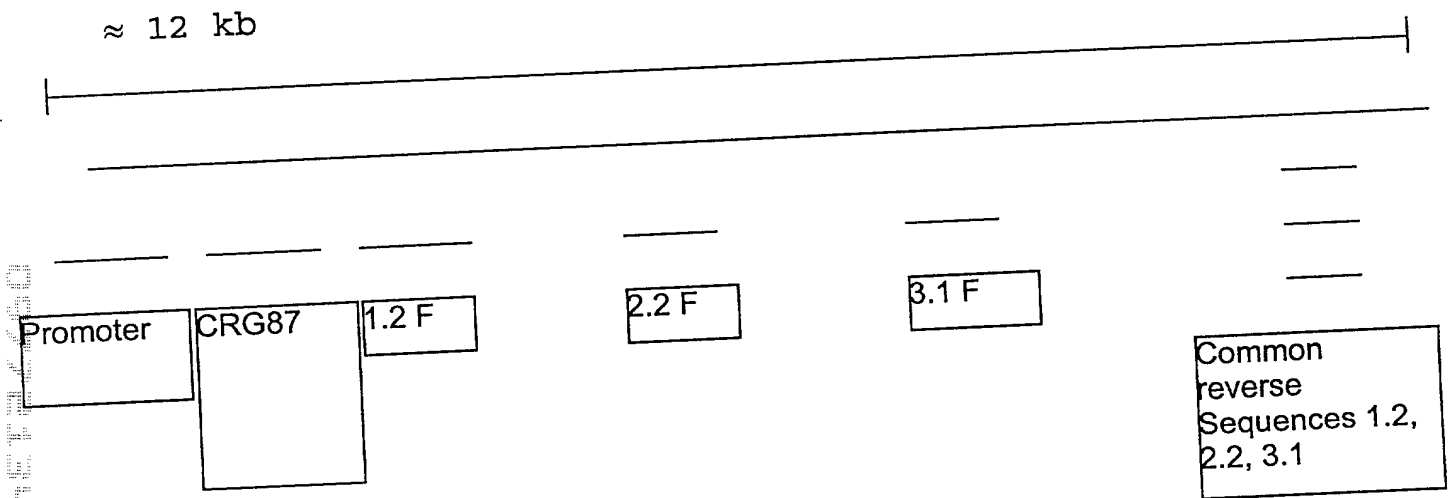
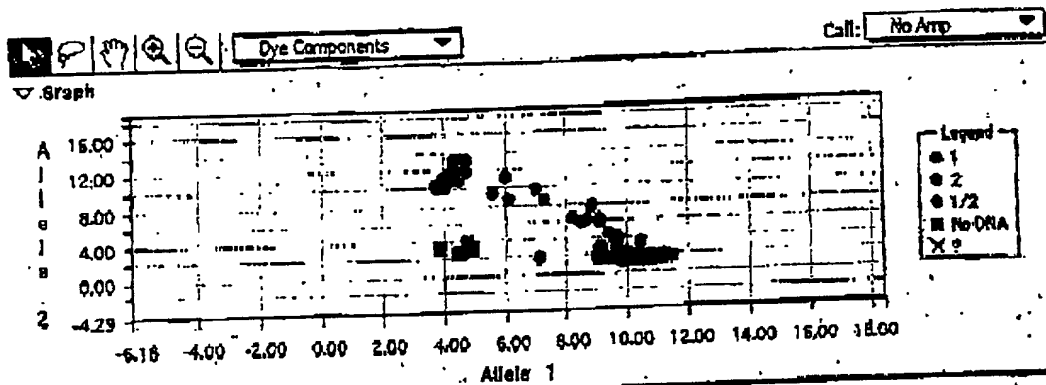


Figure 5



Panel A

Plate

Tray

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	2	1	2	1	1	2	2	1	2	1	2
B	2	1	1	1	1 and 2	1	1	1	1	2	1	2
C	1	1	2	1	1	2	1	2	2	1	1	1
D	1	1	2	2	2	1	2	2	1	1	1	No Amp
E	No Amp	1	2	1	1	No Amp	1	1 and 2	2	1	1	No Amp
F	1	1	1	1	1	1	1	1	2	2	2	No Amp
G	2	1	1 and 2	1	2	1	1	1	1	1	1	No Amp
H	1	1	1	1	1	1	1	2	1	1 and 2	1 and 2	

Panel B

Figure 6

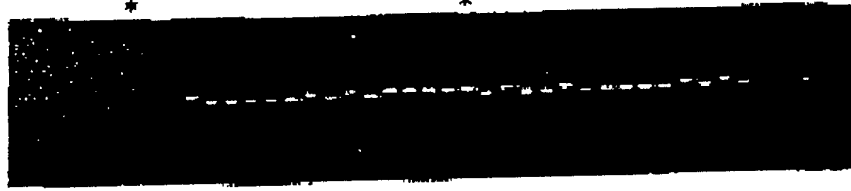
6

Panel A

EF

RILs 1-38

FE



Panel B

RILs 39-78

FE

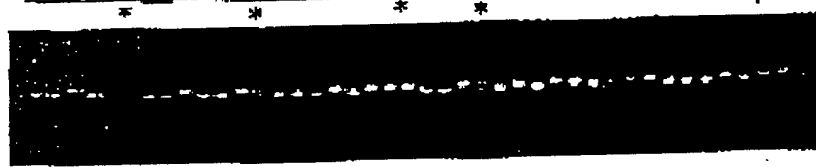


Figure 7A

Synthetic rhg1 gene

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AATGGGAGGAGTGGGAAAGACAGTGGCTATGGAGCTTGTTCCGGAGGTTGGGTTGGAAT
CAAGTGTGCTCAGGGACAGGTTATTGTGATCCAGCTTCCTTGGAAGGGTTTGAGGGGTC
GAATCACCGACAAAAATTGGCCAACTTCAAGGCCTCAGGAAGCTTAGTCTTCATGATAAC
CAAATTGGTGGTTCAATCCCTTCAACTTTGGGACTTCTTCCCAACCTTAGAGGGGTTCA
GTTATTCAACAATAGGCTTACAGGTTCCATACCTCTTTCTTTAGGTTTCTGCCTTTGCT
TCAAGTCTCTTGACCTCAGCAACAACCTTGCTCACAGGAGCAATCCCTTATAGTCTTGCT
AATTCCTAAGCTTTATTGGCTTAACCTTGAGTTTCAACTCCTTCTCTGGTCCTTTACC
AGCTAGCCTAACTCACTCATTTTCTCTCACTTTTCTTCTCTTCAAATAACAATCTTT
CTGGCTCCCTTCCTAACTCTTGGGGTGGGAATCCAAGAATGGCTTCTTTAGGCTTCAA
AATTTGATCCTAGATCATAACTTTTTCACTGGTGACGTTCTGCTTCTTTGGGTAGCTT
AAGAGAGCTCAATGAGATTTCCCTTAGTCATAATAAGTTTAGTGGAGCTATACCAAATG
AAATAGGAACCCTTTCTAGGCTTAAGACACTTGACATTTCTAATAATGCCTTGAATGGG
AACTTGCCCTGCTACCCTCTCTAATTTATCCTCACTTACACTGCTGAATGCAGAGAACAA
CCTCCTTGACAATCAAATCCCTCAAAGTTTAGGTAGATTGCGTAATCTTTCTGTTCTGA
TTTTGAGTAGAAACCAATTTAGTGGACATATTCCTTCAAGCATTGCAAACATTTCTCG
CTTAGGCAGCTTGATTTGTCACTGAATAATTTCACTGGAGAAATTCAGTCTCTCTTTGA
CAGTCAGCGCAGTCTAAATCTCTTCAATGTTTCTTACAATAGCCTCTCAGGTTCTGTCC
CCCCTCTGCTTGCCAAGAAATTTAACTCAAGCTCATTTGTGGGAAATATTTCAACTATGT
GGGTACAGCCCTTCAACCCCATGTCTTTCCCAAGCTCCATCACAAGGAGTCATTGCCCC
ACCTCCTGAAGTGTCAAACATCACCATCATAGGAAGCTAAGCACCAAAGACATAATTC
TCATAGTAGCAGGAGTTCTCCTCGTAGTCCTGATTATACTTTGTTGTGTCTGCTTTTC
TGCCTGATCAGAAAGAGATCAACATCTAGGCCGGGAACGGCCAAGCCACCCGAGGGTAG
AGCGGCCACTATGAGGACAGAAAAAGGAGTCCCTCCAGTTGCTGGTGGTGTGTTGAAG
CAGGTGGGGAGGCTGGAGGGAACTAGTCCATTTTGATGGACCAATGGCTTTTACAGCT
GATGATCTCTTGTGTGCAACAGCTGAGATCATGGGAAAGAGCACCTATGGAAGTGTGTTA
TAAGGCTATTTTGGAGGATGGAAGTCAAGTTGCAGTAAAGAGATTGAGGGGAAAGATCA
CTAAAGGTCATAGAGAATTTGAATCAGAAGTCAGTGTCTAGGAAAAATTAGACACCCC
AATGTTTTTGGCTCTGAGGGCCTATTACTTGGGACCCAAAGGGGAAAGCTTCTGGGTTT
TGATACATGTCTAAAGGAAGTCTTGCTTCTTCTTCTACATGGAAGGTTCTGTGTGCTGGT
CTTTCATTAAAGTGTGTGTGTGCTGGTCTTTAATTATAATTGGAGTTTTACCTTAGT
AATCTGTATAATTCTAATCGGAGAACAGTACAAACAAAAACACCTAAGGAACAACACCT
TANCTTTAATATACCATATCAATAAAGTGAAATATTTTCTTGGTCATCTTGATGCAGGG
GGAAGTGAACATTCAATTATTGGCCACAAGATTAAATAGCCCAAGCCTTGCCCCGGGCT
TGTTTGCCTTCATTCCCAGGAGAACATCATACTGGGACCTCNCATCCAGCAATGTGTG
GCTTGATGAAAAACAAATGCTAAATTCAGATTTTGGTCTTTTTCGGGTTGATGTCAAC
TGCTGCTAATTTCAACGTGATAGCTACAGCTGGAGCATTGGATACCGGGCACCTGAGCT
CTCAAAGCTCAAGAAAGCAAACACTAAACTGATATCTACAGTCTTGGTGTATCTTGT
TAGAACTCCTAACGAGGAAATCACCTGGGGTGTCTATGAATGGACTAGATTTGCCTCAG
TGGGTTGCCTCAGTTGTCAAAGAGGAGTGGACAAATGAGGTTTTTGATGCAGACTTGAT
GAGAGATGCATCCACAGTTGGCGACGAGTTGCTAAACACGTTGAAGCTCGCTTTGCACT
GTGTTGATCCTTCTCCATCAGCACGACCAGAAGTTCATCAAGTTCTCCAGCAGCTGAAG
AGATTAGACCAGAGAGATCAGTCACAGCCAGTCCCGGGGACGATATCGTATAGCACAAA
TTTTGCATTGATTTTTTTGTGCCAAATGTAGTAGGCCTACTATATATATGTTCTATGAT

Figure 7B

TCTTTCATTCTTATATTATTTTTGCCTGTTTGAATGCTTGAATTTGTACATACTCATAC
TACAATAAGGTGTAGTTCTGGTTAATTTTACCTCTACCTCAAAGCTGGGGTGTAATTCT
GTTTCCTCCAAGGCACATAATAGTTGAAAATAGTTCTCAGGAGCATTTCATTGTTTATTC
TGCAAGATTCTCTTTCACGGCTGCTATCTTCTATGCATGCCCTGCCCAT**TAAAT**GCATTA
TGAAGAATTGTAACGGCTGTGTTTTTGGACTTCTTCAAAAAGTTTATGTTATTGCCAGG
TGTATATATCAACATGTTTTTAAAGATTTTCAAACAATCAGGTTTTAGATGTGGGTTTTGC
ATGCATGAGATTGGACTAGTGCCTTGATGTAGTATAAAATAT**TAAAT**TGTCCAATCAAG
CACCTCTACATGTCCAAATAATGGGCCTTATGAACTTAATTTTTTAATTACAACTA
CAGTAATCTTTTTGAATAAAGATTTACAAATTACAACNGACATGTGAAGCNGCATCTTT
NATTGNCAATCTTTCAGTTACTCTATTATTTTCTGCN

3105bp

3105bp

Figure 7C

Rhg1 Peptide

NGRSGKDSGYGAC**SGGW**GIKCAQGQVIVIQLPWKGLRGRIT
DKIGQLQGLRKL**SL**HDNQIGGS**IP**STLGLLPNLRGVQLFNNRLG
SIP
LSLGFCPLLQSLDLSNNLLTGAIP
YSLANSTKLYWLNL**SFNSFSGPLP**
ASLTHSFSLTFLSLQNNNL**SGSLPNSWGG**
NSKNGF**FRLQNL**ILDHNFFTGDVP
ASLGSLRELNEI**SLSHNKFSGAIP**
NEIGT**LSRLK**TLDI**SNNALNGNLP**
ATLSNLSSLTLLNAENNLLDNQIP
QSLGRLRNLSVLILSRNQFSGHIP
SSIANISSLRQLDLSLNNFSGEIP
VSFDSQRSLNLSNVSYNSLSGSVP

PLLAKKFNSSSFVGNIQLCGYSP
STPCLSQ
APSQGVIAAPPPEVSKHHHHR
KLSTKDIILIVAGVLLVVLIIILCCVLLFCLIRKRS
TSKAGNGQATEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHF
DGPMAFTADDLLCATAEIMGKSTYGT**VYKAILEDGSQVAVKRLR**
EKITKGHREFESEVSVLGKIRHPNGLALRAYYLGPKEKLLVFD
YMSKGGLLLFYMEGSCAGSFIKVLCVLVFNYNLEFYLSNLYNSN
RRTVQTKTPKEQHLXFNIPYQ
-SEIFSWSS-CRGN-TFIIGHKMKIXQDLAVACSPSPFETSYMD
LXSSNVCX-NXMLKLQFWSFSVDVNCC-FQRDSYSWSIGIPGT-
ALKAQESKH-N-YLQSWCYLVRT**PNEEITWGVYEWTRFASVGCL**
SCQRGVDK-GF-CRLDERCIHSWRRVAKHVEARFALC-SFSIS
TTRSSSSSPAAGRD-TREISHSQSHLPGRPLEPYSESY

Figure 7D

Sequences producing significant alignments:		Score (bits)	E Value
pir:T46070	hypothetical protein T18N14.120 - Arabidopsis thaliana	632	e-180
pir:T47727	hypothetical protein F18O21.60 - Arabidopsis thaliana	344	1e-95
pir:T04587	hypothetical protein F23E13.70 - Arabidopsis thaliana	268	9e-71
pir:T49038	hypothetical protein T5P19.20 - Arabidopsis thaliana	257	2e-67
pir:T48210	hypothetical protein T20L15.160 - Arabidopsis thaliana	241	1e-62
pir:T05050	protein kinase homolog M3E9.30 - Arabidopsis thaliana	238	2e-61
pir:T18536	receptor-like protein kinase - Ipomoea nil (Japanese...	236	3e-61
pir:T48489	receptor-like protein kinase - Arabidopsis thaliana	236	5e-61
pir:T10515	disease resistance protein Cf-2.2 - currant tomato	235	6e-61
pir:T10504	disease resistance protein Cf-2.1 - currant tomato	235	6e-61
pir:T30553	disease resistance protein Hcr2-5D - tomato	229	4e-59
pir:S27756	receptor-like protein kinase 5 (EC 2.7.1.-) precurs...	227	1e-58
pir:T48499	receptor-like protein kinase-like protein - Arabidop...	226	3e-58
pir:T46033	receptor protein kinase-like protein - Arabidopsis t...	226	4e-58
pir:T05335	hypothetical protein F1C12.190 - Arabidopsis thaliana	221	1e-56
pir:T10636	hypothetical protein T13K14.100 - Arabidopsis thaliana	219	7e-56
pir:T05898	hypothetical protein F6H11.170 - Arabidopsis thaliana	218	1e-55
pir:T45717	receptor-kinase like protein - Arabidopsis thaliana	212	7e-54
pir:T05322	hypothetical protein F18F4.240 - Arabidopsis thaliana	211	1e-53
pir:T10659	probable serine/threonine-specific protein kinase (E...	211	2e-53
pir:T03784	probable receptor protein kinase - rice	208	1e-52
pir:T50851	receptor protein kinase homolog [imported] - soybean	201	1e-50
pir:T45647	receptor protein kinase-like protein - Arabidopsis t...	199	5e-50
pir:T45718	receptor-kinase like protein - Arabidopsis thaliana	199	7e-50
pir:T50850	receptor protein kinase homolog [imported] - soybean	199	7e-50
pir:T45645	receptor kinase-like protein - Arabidopsis thaliana	196	3e-49
pir:T09356	brassinosteroid-insensitive protein BRI1 - Arabidops...	196	3e-49
pir:T00712	protein kinase homolog F22O13.7 - Arabidopsis thaliana	190	2e-47
pir:A57676	protein kinase Xa21 (EC 2.7.1.-), receptor type prec...	190	3e-47
pir:S39476	kinase-like transmembrane protein TMKL1 precursor - ...	188	1e-46
pir:T02154	protein kinase homolog T1F15.2 - Arabidopsis thaliana	188	1e-46
pir:T10725	protein kinase Xa21 (EC 2.7.1.-) A1, receptor type -...	186	5e-46
pir:T05897	protein kinase homolog F6H11.160 - Arabidopsis thaliana	184	1e-45
pir:T04313	protein kinase Xa21 (EC 2.7.1.-), receptor type - rice	183	3e-45
pir:T10727	protein kinase Xa21 (EC 2.7.1.-) D, receptor type - ...	181	2e-44

Figure 7E

>pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana
Length = 836

Score = 632 bits (1613), Expect = e-180
Identities = 329/550 (59%), Positives = 400/550 (71%), Gaps = 2/550 (0%)
Frame = +1

Query: 7 RSGKDSGYGACSGGWVGKCAQGQVIVIQLPWKGLRGRITDKIGQLQGLRKLKSLHDNQIG 186
+S +S GW GIKC +GQV+ IQLPWKGL G I++KIGQL LRKLSLH+N I
Sbjct: 72 KSWNNSASSQVCSGWAGIKCLRQGVVAIQLPWKGLGGTISEKIGQLGSLRKLKSLHNNVIA 131

Query: 187 GSIPSTLGLLPNLRGVQLFNNRLTGSIPSLSLGFCLCFKSLDLSNNLLTGAIPYSLANSTK 366
GS+P +LG L +LRGV LFNRL+GSIP+SLG C ++LDLS+N LTGAIP SL ST+
Sbjct: 132 GSVPRSLGYLKSRLRGVYLFNNRLSGSIPVSLGNCPLLQNLDLSSNQLTGAIPPSLTESTR 191

Query: 367 LYWLNLFSNFSFSGPLPASLTHSFSLTFLSLQNNNLSGSLPNSWGGNSKNGFFRLQNLILD 546
LY LNLFSNFS SGPLP S+ S++LTFL LQ+NNLSGS+P+ + NG L+ L LD
Sbjct: 192 LYRLNLFSNLSGPLPVSVARSYTLTFLDLQHNNLSGSIPDFF---VNGSHPLKTLNLD 247

Query: 547 HNFFTGDVPASLGSLRELNEISLSHNKFSGAIPNEIGTSLRKTLDISNNALNGNLPATL 726
HN F+G VP SL L E+S+SHN+ SG+IP E G L L++LD S N++NG +P +
Sbjct: 248 HNRFSGAVPVSLCKHSLLEEVSISHNQLSGSIPRECGLPHLQSLDFSYSINGTIPDSF 307

Query: 727 SNLSSLTLLNAENNLLDNQIPQSLGRLRLSVLILSRNQFSGHIPSSIANISSLRQLDLS 906
SNLSSL LN E+N L IP ++ RL NL+ L L RN+ +G IP +I NIS +++LDLS
Sbjct: 308 SNLSSLVSLNLESNHLKGPIPDALDRHLNLTLENLKRNKINGPIPETIGNISGIKKDLS 367

Query: 907 LNNFSGEIPVSFDSQSRSLNLFNVSYNSLSGSPVPLLAKKFNSSSFVGNQLCGYSPSTPC 1086
NNF+G IP+S L+ FNVSYN+LSG VPP+L+KKFNSSSF+GNIQLCGYS S PC
Sbjct: 368 ENNFTGPIPLSLVHLAKLSSFNVSYNLTLGPPVPLSKKFNSSSFGLNIQLCGYSSNPC 427

Query: 1087 LSQAPSQGVIAAPP--PEVSKHHHHRKLS TKDIILIVAGVLLVVLIIILCCVLLFCLIRKRS 1260
+ + P + + HHHRKLS KD+ILI G LL +L++LCC+LL CLI+KR+
Sbjct: 428 PAPDHHHPLTSLPTSSQEPRKHHHHRKLSVKDVILIAIGALLAILLLLCCILLCCLIKRA 487

Query: 1261 TSRPGTAKPPEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHFDGPMFTAADDLLCATA 1440
K +G+ T +EK V G AGGE GGKLVHFDGP FTADDLLCATA
Sbjct: 488 -----ALKQKDGKDKT--SEKTVSAGVAGTASAGGEMGGKLVHFDGPFVFTAADDLLCATA 540

Query: 1441 EIMGKSTYGT VYKAILEDGSQVAVKRLREKITKGHREFESEVSVLGKIRHPNVLALRAYY 1620
EIMGKSTYGT YKA LEDG++VAVKRLREK TKG +EFE EV+ LGKIRH N+LALRAYY
Sbjct: 541 EIMGKSTYGTAYKATLEDGNEVAVKRLREKTTKGVKEFEGETALGKIRHQNLALRAYY 600

Query: 1621 LGPKGEKLLGFD 1656
LGPKGEKLL FD
Sbjct: 601 LGPKGEKLLVFD 612

Figure 7F

Score = 185 bits (464), Expect = 1e-45
Identities = 93/161 (57%), Positives = 122/161 (75%), Gaps = 3/161 (1%)
Frame = +2

Query: 1943 GLVCLHSQENIIHGTSHPAMCGLMKNKC*NS--DFGLFRVDVNCC*FQRDSYSWSIGYR 2113
GL LHS EN+IH + ++ ++ N+ D+GL R+ + + ++GYR
Sbjct: 647 GLAHLHSNENMIH--ENLTASNILLDEQTNADIYGLSRLMTAAAATNVIATAGTLGYR 704

Query: 2114 APELSKLLKANTKTDIYSLGVILLELLTRKSPGVSMNGLDLPQWVASVVKEEWTNEVFDA 2293
APE SK+K A+ KTD+YSLG+I+LELLT KSPG NG+DLPQWVAS+VKEEWTNEVFD
Sbjct: 705 APEFSKIKNASAKTDVYSLGIIILELLTGKSPGEPTNGMDLPQWVASIVKEEWTNEVFDL 764

Query: 2294 DLMRDASTVGDELLNTLKLALHCVDPSPSARPEVHQVLQQLKRL 2425
+LMR+ +VGDELLNTLKLALHCVDPS+ARPE +QV++QL+ +
Sbjct: 765 ELMRETQSVGDELLNTLKLALHCVDPSPAARPEANQVVEQLEEI 808

Query: 1943 GLVCLHSQENIIHGTSHPAMCGLMKNKC*NS--DFGLFRVDVNCC*FQRDSYSWSIGYR 2113
GL LHS EN+IH + ++ ++ N+ D+GL R+ + + ++GYR
Sbjct: 647 GLAHLHSNENMIH--ENLTASNILLDEQTNADIYGLSRLMTAAAATNVIATAGTLGYR 704

Query: 2114 APELSKLLKANTKTDIYSLGVILLELLTRKSPGVSMNGLDLPQWVASVVKEEWTNEVFDA 2293
APE SK+K A+ KTD+YSLG+I+LELLT KSPG NG+DLPQWVAS+VKEEWTNEVFD
Sbjct: 705 APEFSKIKNASAKTDVYSLGIIILELLTGKSPGEPTNGMDLPQWVASIVKEEWTNEVFDL 764

Query: 2294 DLMRDASTVGDELLNTLKLALHCVDPSPSARPEVHQVLQQLKRL 2425
+LMR+ +VGDELLNTLKLALHCVDPS+ARPE +QV++QL+ +
Sbjct: 765 ELMRETQSVGDELLNTLKLALHCVDPSPAARPEANQVVEQLEEI 808